



SEQUENCE LISTING

<110> REGEN Biotech. Inc.

<120> The method for measuring the amount of Betaig - h 3 protein and diagnostic kit using the same

<130> 2fpo-10-14

<160> 12

<170> KopatentIn 1.71

<210> 1

<211> 683

<212> PRT

<213> Homo sapiens

<400> 1

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Gly Pro Ala Ala Thr Leu Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu
20 25 30

Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val
35 40 45

Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn
50 55 60

Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile
65 70 75 80

Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly
85 90 95

Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val
100 105 110

Val Gly Ser Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu
115 120 125

Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser
130 135 140

Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val
145 150 155 160

Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val
 165 170 175

 Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr
 180 185 190

 Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly
 195 200 205

 Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala
 210 215 220

 Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr
 225 230 235 240

 Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu
 245 250 255

 Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn
 260 265 270

 Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile
 275 280 285

 Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg
 290 295 300

 Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala
 305 310 315 320

 Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu
 325 330 335

 Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile
 340 345 350

 Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp
 355 360 365

 Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala
 370 375 380

 Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu
 385 390 395 400

 Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu
 405 410 415

 Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg

420	425	430
Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr		
435	440	445
Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg		
450	455	460
Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala		
465	470	475
Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg		
485	490	495
Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp		
500	505	510
Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr		
515	520	525
Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn		
530	535	540
Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly		
545	550	555
Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu		
565	570	575
Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu		
580	585	590
Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val		
595	600	605
Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val		
610	615	620
Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln		
625	630	635
Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln		
645	650	655
Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Pro		
660	665	670
Val Tyr Gln Lys Leu Leu Glu Arg Met Lys His		
675	680	

<210>	2					
<211>	2691					
<212>	DNA					
<213>	Homo sapiens					
<400>	2					
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ccgccaagtc	gccctaccag	ctggtgctgc	agcacagcag	gctccgggc	cgccagcacg	180
gccccaacgt	gtgtgctgtg	cagaaggta	ttggcactaa	taggaagtac	ttcaccaact	240
gcaaggcagt	gtaccaaagg	aaaatctgtg	gcaaatcaac	agtcatcagc	tacgagtgt	300
gtcctggata	tgaaaagg	tc	ctggggaga	agggctgtcc	agcagcccta	360
acctttacga	gaccctgg	gtcg	ttggat	ccaccac	ttagctgtac	420
cg	gagaagct	gaggc	ctgag	atggaggg	ccggc	480
acgaggc	ctg	ggc	cttgc	ccag	ctgtc	540
ttgag	ctg	aat	gccc	ccata	tggggcag	600
tgaa	acac	cg	ccct	atgt	gctc	660
atc	cta	atgg	ttgg	actgt	gtgt	720
cca	acgg	gtgc	ccct	atcg	atcc	780
agat	catt	gatc	tttg	accc	acc	840
tca	acac	gatc	ggcc	acac	ccgc	900
tcg	agaag	ccct	atgt	gttt	gggc	960
ac	ttgt	actt	gtgg	ccat	ccat	1020
tgt	ctgt	gtat	ccgg	catc	gttgc	1080
ctat	caac	ccat	gggc	acac	gggg	1140
acta	catt	tgag	ccat	caga	gtat	1200
agt	ctgt	actc	ccat	ccat	ccat	1260

ctggaaagtga	gcgggttgacc	ctcctggctc	ccctgaattc	tgtattcaaa	gatggAACCC	1320
ctccaattga	tgcccataaca	aggaatttgc	ttcggAACCA	cataattaaa	gaccagctgg	1380
cctcttaagta	tctgtaccat	ggacagACCC	tggAAactct	gggcggcaaa	aaactgagag	1440
tttttgttta	tcgtaatAGC	ctctgcattg	agaacagACTG	catcgCGGCC	cacgacaaga	1500
gggggaggta	cgggaccctg	ttcacgatgg	accgggtgct	gacccccc	atggggactg	1560
tcatggatgt	cctgaaggga	gacaatcgct	ttagcatgct	ggtagctgcc	atccagtc	1620
caggactgac	ggagaccctc	aaccgggaag	gagtctacac	agtctttgct	cccacaatg	1680
aagccttccg	agccctGCCA	ccaagagaac	ggagcagact	cttgggagat	gccaaGGAAC	1740
ttgccaacat	cctgaaatac	cacattggtg	atgaaatcct	ggttagcgga	ggcatcgGGG	1800
ccctggtgcg	gctaaagtct	ctccaagggt	acaagctgga	agtcaGCTTG	aaaaacaatg	1860
tggtgagtgt	caacaaggag	cctgttgccg	agcctgacat	catggccaca	aatggcgtgg	1920
tccatgtcat	caccaatgtt	ctgcagcctc	cagccaaacag	acctcaggaa	agaggggatg	1980
aacttgcaga	ctctgcgcTT	gagatctca	aacaagcatc	agcgTTTCC	agggcttccc	2040
agaggtctgt	gcgactAGCC	cctgtctatc	aaaagttatt	agagaggatg	aagcattAGC	2100
ttgaaggact	acaggaggaa	tgcaccacgg	cagctctccg	ccaatttctc	tcagatttcc	2160
acagagactg	tttgaatgtt	ttcaaaacca	agtatcacac	tttaatgtac	atgggcccga	2220
ccataatgag	atgtgagcct	tgtgcattgt	ggggaggagg	gagagagatg	tactttttaa	2280
atcatgttcc	ccctaaacat	ggctgttaac	ccactgcatt	cagaaacttg	gatgtcactg	2340
cctgacatTC	acttccagag	aggacctatc	ccaaatgtgg	aattgactgc	ctatGCCAG	2400
tccctggaaa	aggagcttca	gtattgtgg	gctcataaaa	catgaatcaa	gcaatccAGC	2460
ctcatggaa	gtcctggcac	agttttgtta	aagcccttgc	acagctggag	aaatggcatc	2520
attataagct	atgagttgaa	atgttctgtc	aaatgtgtct	cacatctaca	cgtggcttgg	2580
aggctttat	ggggccctgt	ccaggtagaa	aagaaatggt	atgtagagct	tagatttccc	2640
tattgtgaca	gagccatgg	gtgtttgtaa	taataaaacc	aaagaaacat	a	2691

<210> 3
 <211> 585
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)...(585)
 <223> 69 to 653 amino acid sequence of human ID No.1

<400> 3

Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile Ser Tyr Glu Cys
 1 5 10 15

Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly Cys Pro Ala Ala
 20 25 30

Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr
 35 40 45

Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met
 50 55 60

Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp
 65 70 75 80

Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn
 85 90 95

Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val
 100 105 110

Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln
 115 120 125

Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val
 130 135 140

Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val
 145 150 155 160

Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln
 165 170 175

Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val
 180 185 190

Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn Gly Gln Tyr Thr
 195 200 205

Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile Pro Ser Glu Thr
 210 215 220

Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg Asp Leu Leu Asn
 225 230 235 240

Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala Ile Val Ala Gly
 245 250 255

Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu Val Gly Cys Ser
 260 265 270

Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile Ser Asn Lys Asp
 275 280 285

Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp Glu Leu Leu Ile
 290 295 300

Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala Glu Ser Asp Val
 305 310 315 320

Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu Gly Asn His Leu
 325 330 335

Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu Asn Ser Val Phe
 340 345 350

Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg Asn Leu Leu Arg
 355 360 365

Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr Leu Tyr His Gly
 370 375 380

Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg Val Phe Val Tyr
 385 390 395 400

Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala Ala His Asp Lys
 405 410 415

Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg Val Leu Thr Pro
 420 425 430

Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser
 435 440 445

Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn

450	455	460
Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg		
465	470	475
Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu		
485	490	495
Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser		
500	505	510
Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys		
515	520	525
Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro		
530	535	540
Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile		
545	550	555
His Val Ile		
560		
Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln Glu Arg Gly Asp		
565	570	575
Glu Leu Ala Asp Ser Ala Leu Glu Ile		
580	585	

<210>	4					
<211>	1857					
<212>	DNA					
<213>	Mouse Intracisternal A-particle					
<400>	4					
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accaactgca	agcagtggta	ccagaggaag	atctgcggca	agtgcacagt	catcagttat	180
gagtgctgtc	ctggatatga	aaaggtccca	ggagagaaaag	gttgcccagc	agctcttccg	240
ctctcaaatc	tgtatgagac	catgggagtt	gtgggatcga	ccaccacaca	gctgtataca	300
gaccgcacag	aaaagctgag	gcctgagatg	gagggacccg	gaagcttcac	catctttgct	360
cctagcaatg	aggcctggtc	ttccttgct	gcggaagtgc	tggactccct	ggtgagcaac	420
gtcaacatcg	aactgctcaa	tgctctccgc	taccacatgg	tggacaggcg	ggtcctgacc	480

gatgagctca	agcacggcat	gaccctcacc	tccatgtacc	agaattccaa	catccagatc	540
catcactatc	ccaatggat	tgtaactgtt	aactgtgcc	ggctgctgaa	ggctgaccac	600
catgcgacca	acggcgtgg	gcatctcatt	gacaaggta	tttccaccat	caccaacaac	660
atccagcaga	tcattgaaat	cgaggacacc	tttgagacac	ttcgggcccgc	cgtggctgca	720
tcaggactca	ataccgtgct	ggagggcgac	ggccagttca	cactcttggc	cccaaccaac	780
gaggccttg	agaagatccc	tgccgagacc	ttgaaccgca	tcctgggtga	cccagaggca	840
ctgagagacc	tgctaaacaa	ccacatcctg	aagtcagcca	tgtgtgctga	ggccattgta	900
gctggaatgt	ccatggagac	cctggggggc	accacactgg	aggtgggctg	cagtgggac	960
aagctcacca	tcaacggaa	ggctgtcattc	tccaacaaag	acatcctggc	caccaacgg	1020
gtcattcatt	tcattgatga	gctgcttatac	ccagattcag	ccaagacact	gcttgagctg	1080
gctgggaat	ctgacgtctc	caactgcccatt	gacatcctca	aacaagctgg	cctcgatact	1140
catctctctg	ggaaagaaca	gttgaccttc	ctggcccccc	tgaattctgt	gttcaaagat	1200
ggtgtccctc	gcatcgacgc	ccagatgaag	actttgcttc	tgaaccacat	ggtcaaagaa	1260
cagttggcct	ccaagtatct	gtactctgga	cagacactgg	acacgctggg	tggaaaaag	1320
ctgcgagtct	ttgttatcg	aaatagcctc	tgcattgaaa	acagctgcat	tgctgcccatt	1380
gataagaggg	gacggtttgg	gaccctgttc	accatggacc	ggatgttgac	accccaatg	1440
gggacagtta	tggatgtcct	gaagggagac	aatcgttta	gcatgctggt	ggccgcccatt	1500
cagtctgcag	gactcatgga	gatcctcaac	cgggaagggg	tctacactgt	ttttgctccc	1560
accaatgaag	cgttccaagc	catgcctcca	gaagaactga	acaaactctt	ggcaaatgcc	1620
aaggaactta	ccaacatcct	gaagtaccac	attggtgatg	aaatcctggt	tagcggaggc	1680
atcggggccc	tggtgccgct	gaagtctctc	caaggggaca	aactggaagt	cagctcgaaa	1740
aacaatgtag	tgagtgtcaa	taaggagcct	gttgccgaaa	ccgacatcat	ggccacaaac	1800
ggtgtggct	atgccatcaa	caactgttctg	cagccgcccag	ccaaaccgacc	acaagaa	1857

<210> 5

<211> 609

<212> PRT
 <213> Mouse Intracisternal A-particle

 <220>
 <221> PEPTIDE
 <222> (1)..(609)
 <223> 23 to 641 amino acid sequence of mouse

 <400> 5
 Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu Val Leu Gln His Ser Arg
 1 5 10 15

 Leu Arg Gly Arg Gln His Gly Pro Asn Val Cys Ala Val Gln Lys Val
 20 25 30

 Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn Cys Lys Gln Trp Tyr Gln
 35 40 45

 Arg Lys Ile Cys Gly Lys Ser Thr Val Ile Ser Tyr Glu Cys Cys Pro
 50 55 60

 Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly Cys Pro Ala Ala Leu Pro
 65 70 75 80

 Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr Thr Thr
 85 90 95

 Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met Glu Gly
 100 105 110

 Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp Ala Ser
 115 120 125

 Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn Ile Glu
 130 135 140

 Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val Leu Thr
 145 150 155 160

 Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln Asn Ser
 165 170 175

 Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val Asn Cys
 180 185 190

 Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val Val His
 195 200 205

Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln Gln Ile
 210 215 220

Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val Ala Ala
 225 230 235 240

Ser Gly Leu Asn Thr Met Leu Glu Gly Asn Gly Gln Tyr Thr Leu Leu
 245 250 255

Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile Pro Ser Glu Thr Leu Asn
 260 265 270

Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg Asp Leu Leu Asn Asn His
 275 280 285

Ile Leu Lys Ser Ala Met Cys Ala Glu Ala Ile Val Ala Gly Leu Ser
 290 295 300

Val Glu Thr Leu Glu Gly Thr Thr Leu Glu Val Gly Cys Ser Gly Asp
 305 310 315 320

Met Leu Thr Ile Asn Gly Lys Ala Ile Ile Ser Asn Lys Asp Ile Leu
 325 330 335

Ala Thr Asn Gly Val Ile His Tyr Ile Asp Glu Leu Leu Ile Pro Asp
 340 345 350

Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala Glu Ser Asp Val Ser Thr
 355 360 365

Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu Gly Asn His Leu Ser Gly
 370 375 380

Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu Asn Ser Val Phe Lys Asp
 385 390 395 400

Gly Thr Pro Pro Ile Asp Ala His Thr Arg Asn Leu Leu Arg Asn His
 405 410 415

Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr Leu Tyr His Gly Gln Thr
 420 425 430

Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg Val Phe Val Tyr Arg Asn
 435 440 445

Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala Ala His Asp Lys Arg Gly
 450 455 460

Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg Val Leu Thr Pro Pro Met
 465 470 475 480

 Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu
 485 490 495

 Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu
 500 505 510

 Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu
 515 520 525

 Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala
 530 535 540

 Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly
 545 550 555 560

 Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu
 565 570 575

 Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala
 580 585 590

 Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn
 595 600 605

Val

<210> 6
 <211> 391
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Betaig-h3 D-IV

<400> 6
 gtttgggacc ctgttcacca tggaccggat gttgacacccc ccaatgggga cagttatgga 60

 tgtcctgaag ggagacaatc gtttagcat gctggtgcc gccatccagt ctgcaggact 120

 catggagatc ctcaaccggg aaggggtcta cactgtttt gctccacca atgaagcggt 180

 ccaagccatg cctccagaag aactgaacaa actcttgca aatgccaagg aacttaccaa 240

catcctgaag taccacattg gtgatgaaat cctggtagc ggaggcatcg gggccctggt 300
 gcggctgaag tctctccaag gggacaaaact ggaagtcagc tcgaaaaaca atgttagtgag 360
 tgtcaataag gagcctgttg ccgaaaccga c 391

<210> 7
 <211> 140
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Betaig-h3 D-IV(1X) amino acid sequence

<400> 7
 Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn
 1 5 10 15
 Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
 20 25 30
 Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
 35 40 45
 Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
 50 55 60
 Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
 65 70 75 80
 Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
 85 90 95
 Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
 100 105 110
 Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
 115 120 125
 His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn
 130 135 140

<210> 8
 <211> 280
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Betaaig-h3 D-IV(2X) amino acid sequence

<400> 8

Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn
1 5 10 15Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
20 25 30Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
35 40 45Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
50 55 60Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
65 70 75 80Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
85 90 95Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
100 105 110Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
115 120 125His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro
130 135 140Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met
145 150 155 160Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg
165 170 175Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala
180 185 190Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu
195 200 205Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly
210 215 220

Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu

225	230	235	240
Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val			
245	250	255	
Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr			
260	265	270	
Asn Val Leu Gln Pro Pro Ala Asn			
275	280		
<210> 9			
<211> 420			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Betaig-h3 D-IV(3X) amino acid sequence			
<400> 9			
Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn			
1	5	10	15
Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu			
20	25	30	
Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu			
35	40	45	
Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp			
50	55	60	
Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile			
65	70	75	80
Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln			
85	90	95	
Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn			
100	105	110	
Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val			
115	120	125	
His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro			
130	135	140	

Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met
 145 150 155 160

 Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg
 165 170 175

 Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala
 180 185 190

 Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu
 195 200 205

 Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly
 210 215 220

 Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu
 225 230 235 240

 Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val
 245 250 255

 Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr
 260 265 270

 Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro Met Gly Thr Val
 275 280 285

 Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu Val Ala Ala
 290 295 300

 Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr
 305 310 315 320

 Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg
 325 330 335

 Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu
 340 345 350

 Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala
 355 360 365

 Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu Val Ser Leu
 370 375 380

 Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp
 385 390 395 400

 Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln

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Pro Pro Ala Asn
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Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
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Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
 35 40 45

Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
 50 55 60

Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
 65 70 75 80

Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
 85 90 95

Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
 100 105 110

Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
 115 120 125

His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro
 130 135 140

Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met
 145 150 155 160

Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg
 165 170 175

Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala
 180 185 190

 Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu
 195 200 205

 Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly
 210 215 220

 Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu
 225 230 235 240

 Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val
 245 250 255

 Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr
 260 265 270

 Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro Met Gly Thr Val
 275 280 285

 Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu Val Ala Ala
 290 295 300

 Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr
 305 310 315 320

 Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg
 325 330 335

 Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu
 340 345 350

 Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala
 355 360 365

 Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu Val Ser Leu
 370 375 380

 Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp
 385 390 395 400

 Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln
 405 410 415

 Pro Pro Ala Asn Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu
 420 425 430

 Lys Gly Asp Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala

435

440

445

Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala
 450 455 460

Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg
 465 470 475 480

Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile
 485 490 495

Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu
 500 505 510

Lys Ser Leu Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val
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Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr
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Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn
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